Fig. 6 shows a schematic representation of an apparatus in accordance with the present invention for evaluating the sequence of a target polynucleotide. The apparatus as shown comprises a processor housing 10 which has an input 11 for receiving information from a sequencer 12 about one or more experimental DNA sequencing data traces derived from the separation of experimental DNA sequencing fragments reflecting the position of at least one base in the target polynucleotide and one or more reference DNA sequencing data traces derived from the separation of reference DNA sequencing fragments reflecting the position of at least one base in a reference polynucleotide of known sequence. For example, input 11 may be in the form of a wire for transmitting sequence-related data from a sequencer. Data could also be transmitted via a wireless link, or communicated to the apparatus through disk drive 13.

Please delete the last paragraph on page 12 beginning at line 23 and extending through line 2 on page 13 and replace that paragraph with the following paragraph:

Figs. 1 and 2 illustrate the application of the invention to the specific sequences described above. An M13 sequence using T-terminated sequencing fragments was performed with T = 6% and run at 60°C on a long gel with a voltage of 1500v. Fig. 1 shows the spacing between adjacent bases as a function of base number, for non-aligned (raw) data (closed diamonds), and data aligned and linearized using a 3rd order (open triangles) and 5th order (open circles) polynomials. It is clearly seen that the spacing is changing during the run significantly, but is linearized by fitting with either the 3rd or 5th order polynomial.

In the claims:

Please amend the following claims as indicated:

1. (Amended) A method for assignment of base numbers to peaks within one or more experimental DNA sequencing data traces derived from the separation of experimental

2